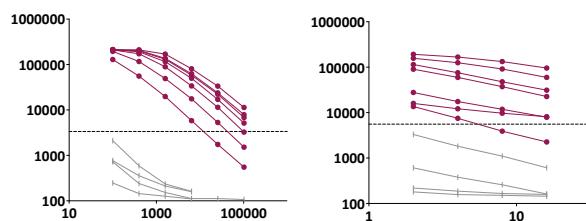
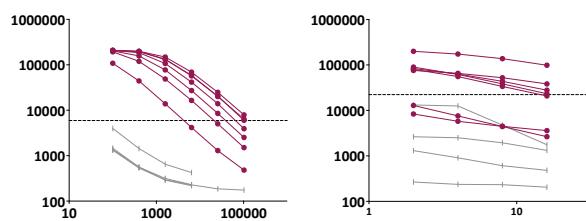




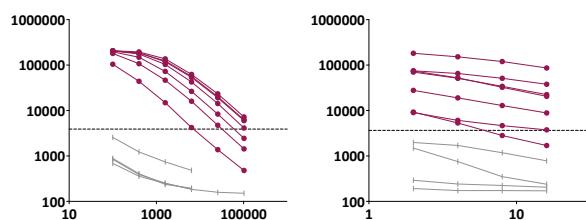
## Spike



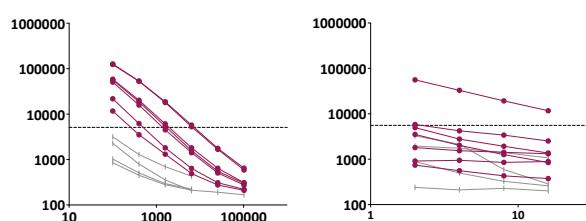
RBD



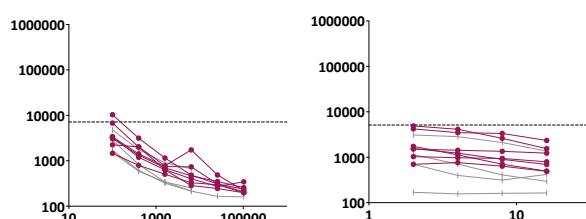
S1



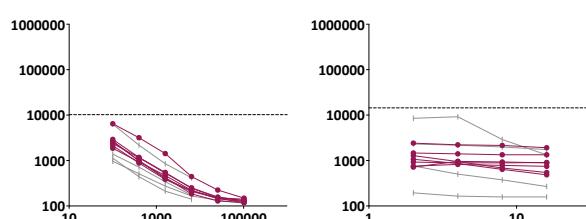
S2



## Nucleoprotein



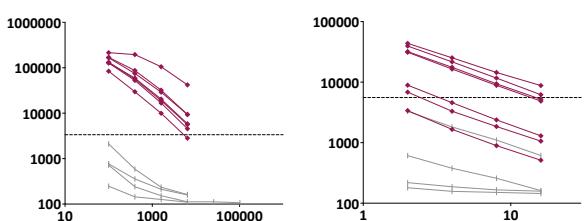
BSA



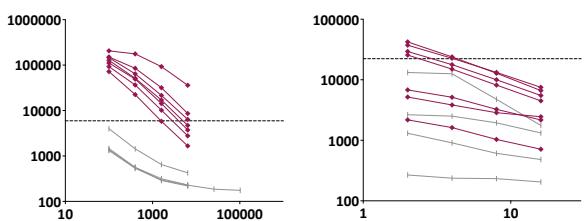
## Plasma dilution

## Saliva dilution

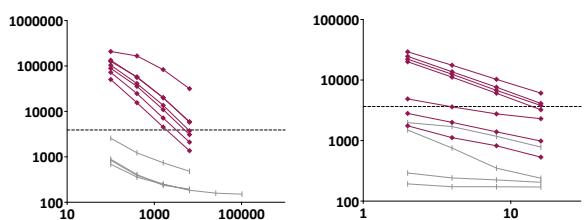
## Spike



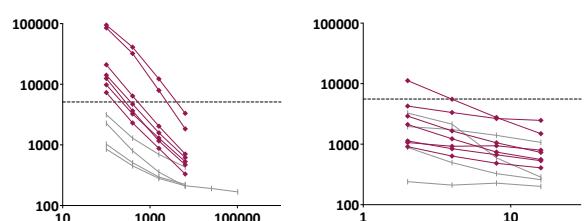
RBD



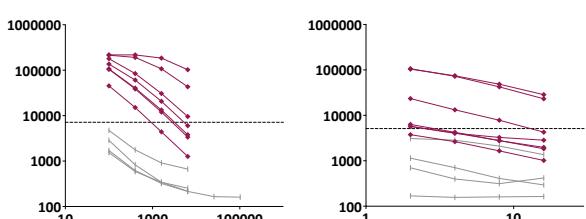
S1



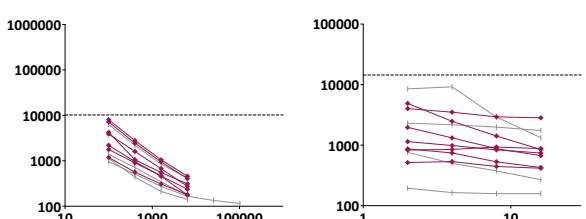
S2



## Nucleoprotein



BSA



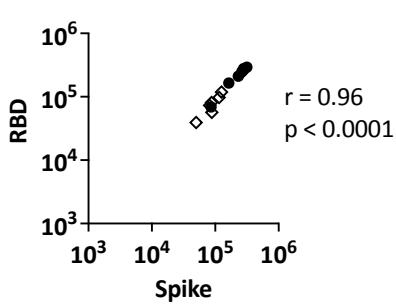
## Plasma dilution

## Saliva dilution

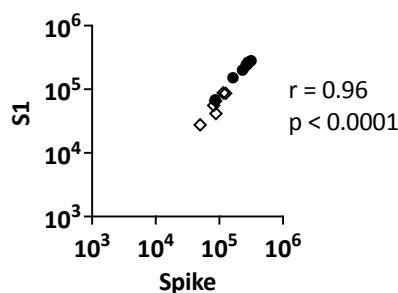
**Supplemental Figure 1.** Titration curves are shown for total Ig against spike, RBD, S1, S2, nucleoprotein (N), and BSA in plasma and saliva specimens from seven vaccinated subjects (left panels), seven convalescent COVID-19 patients (right panels) and four COVID-19-negative subjects (gray). Specimens were diluted at 4-fold dilutions from 1:100 to 1:6,400 or 102,400 (plasma) or 2-fold from 1:2 to 1:16 (saliva). The dotted lines indicated the cut-off values calculated as mean + 3SD of 1:100 diluted plasma or 1:4 diluted saliva of the four COVID-19-negative specimens. Data were generated from the multiplex bead antibody binding assay and mean fluorescent intensity (MFI) values were plotted.

**(A)**

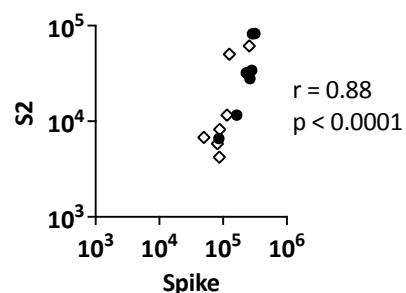
Total Ig AUC - plasma



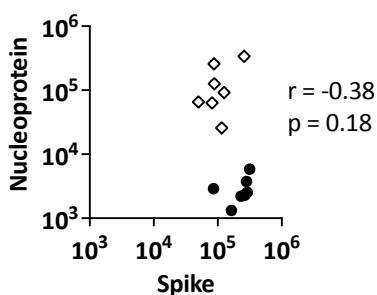
Total Ig AUC - plasma



Total Ig AUC - plasma



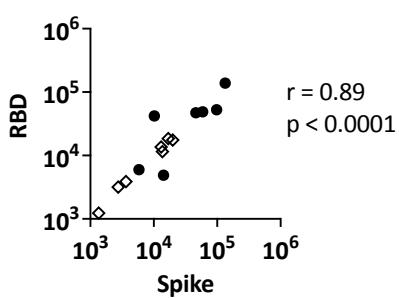
Total Ig AUC - plasma



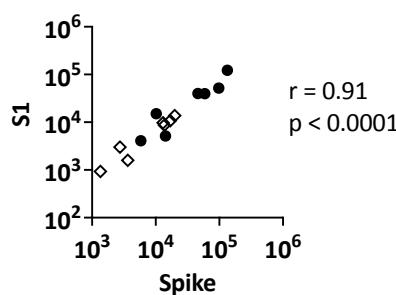
◊ Convalescent COVID-19 patients  
● Vaccinated subjects  
... Cutoff

**(B)**

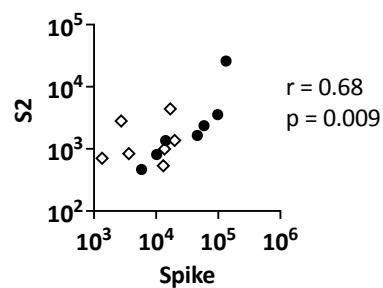
Total Ig AUC - saliva



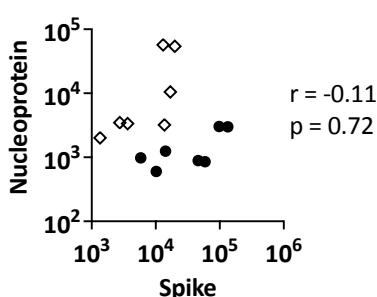
Total Ig AUC - saliva



Total Ig AUC - saliva

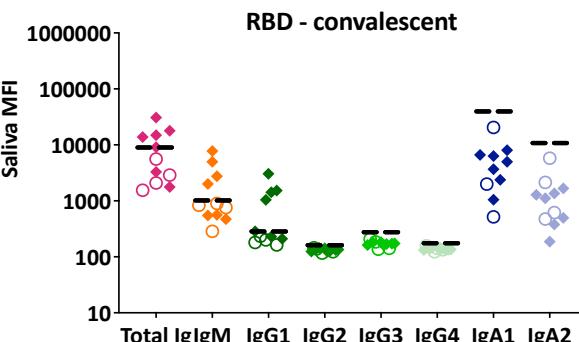
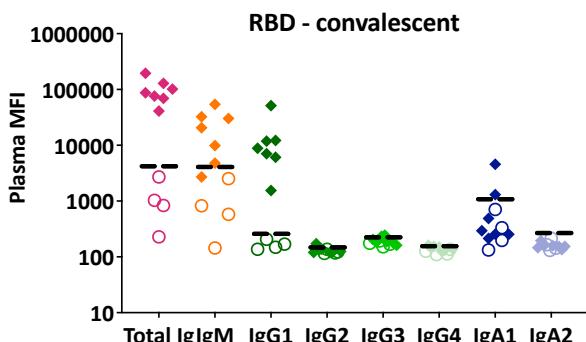
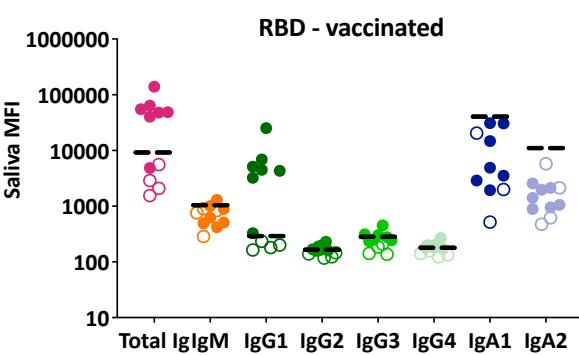
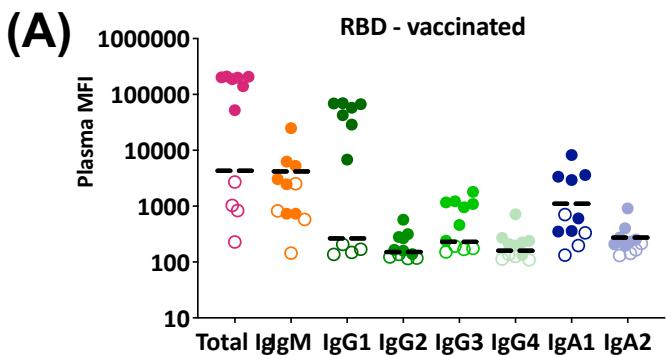


Total Ig AUC - saliva



◊ Convalescent COVID-19 patients  
● Vaccinated subjects  
... Cutoff

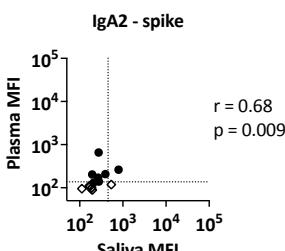
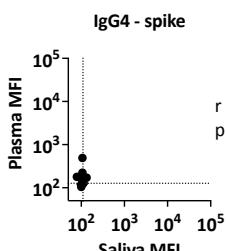
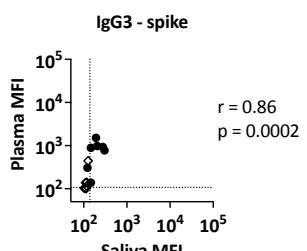
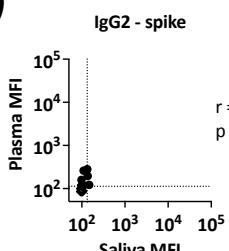
**Supplemental Figure 2.** Spearman correlation of spike- versus RBD-, S1-, S2- or nucleoprotein-specific total Ig levels in (A) plasma or (B) saliva from vaccinated and convalescent subjects.



○ COVID-19-negative subjects

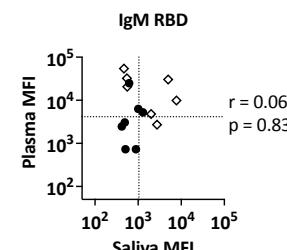
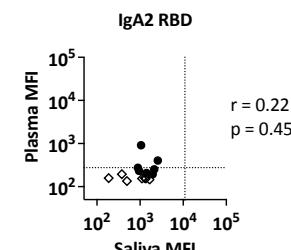
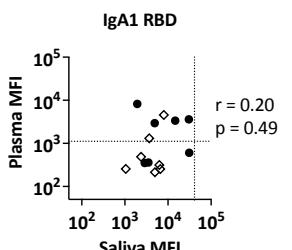
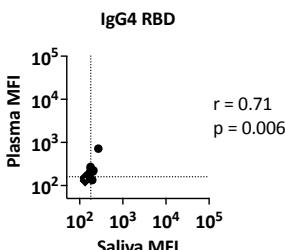
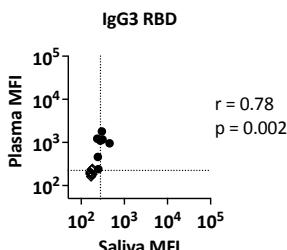
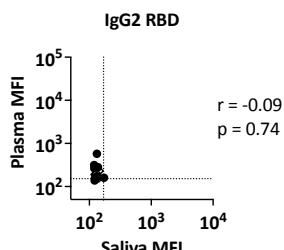
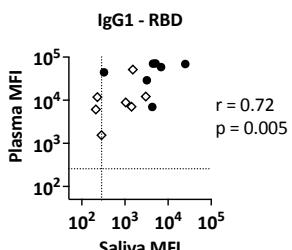
— Cutoff

**(B)**



◊ Convalescent COVID-19 patients  
● Vaccinated subjects  
... Cutoff

**(C)**

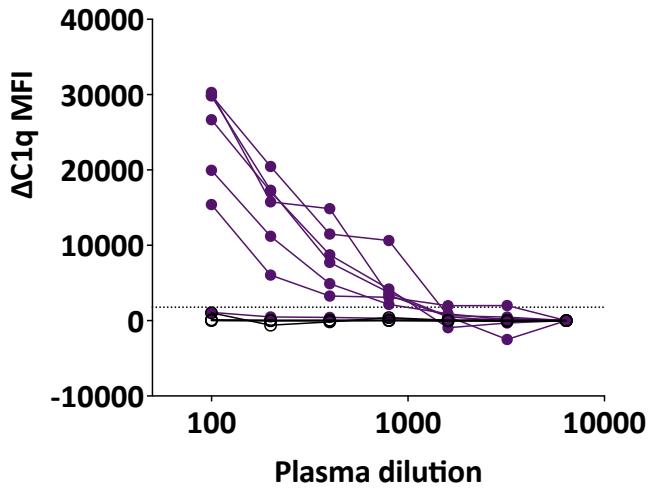


◊ Convalescent COVID-19 patients  
● Vaccinated subjects  
... Cutoff

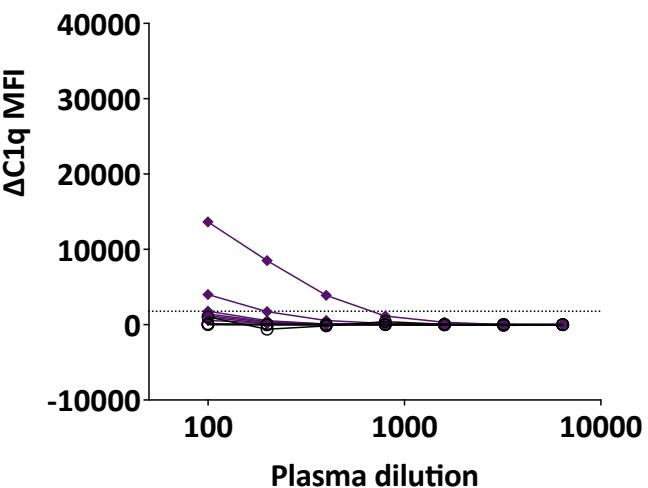
**Supplemental Figure 3.** (A) Total Ig, IgM, IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2 levels against RBD were measured in plasma (left) and saliva (right) specimens from vaccinated (top panel), convalescent COVID-19 patients (lower panel) and COVID-19-negative controls. The dotted line represents the cut-off values calculated as mean of the four control specimens + 3SD for each isotype. (B-C) Spearman correlation of (B) spike- and (C) RBD-specific isotypes levels in plasma versus saliva from vaccinated and convalescent subjects. The dotted line represents the cut-off.

**(A)**

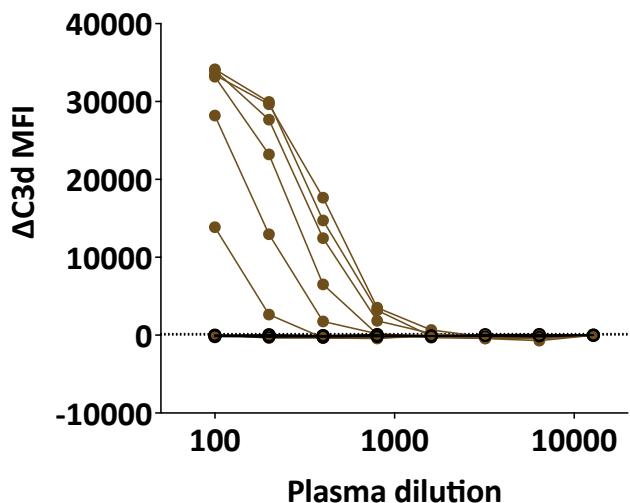
RBD - vaccinated



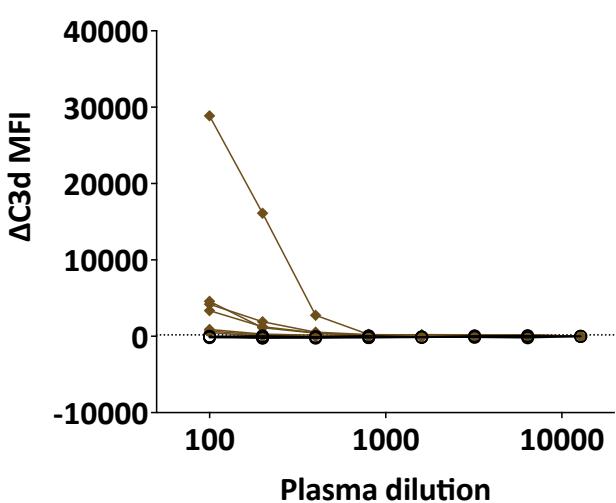
RBD - convalescent

**(B)**

RBD - vaccinated



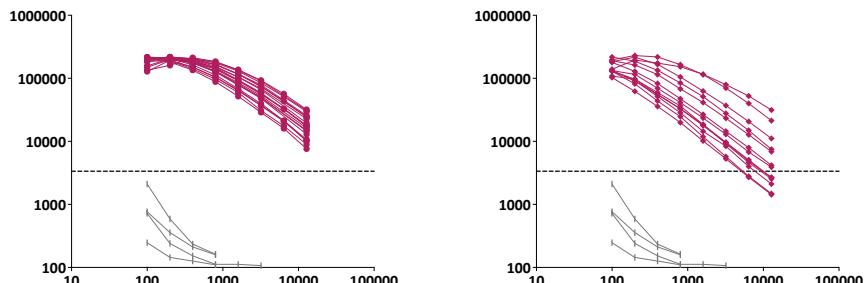
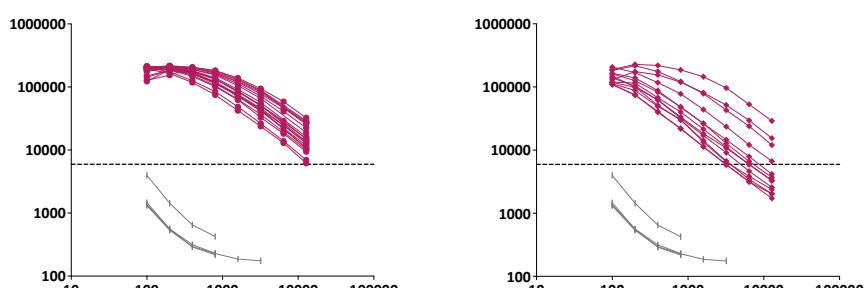
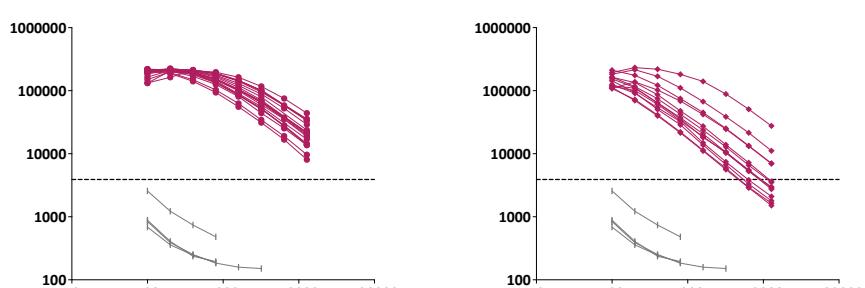
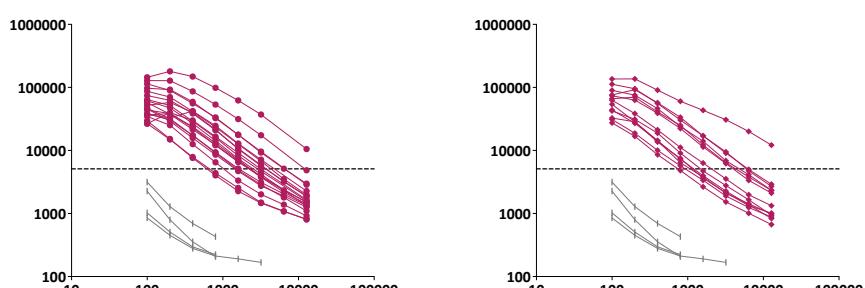
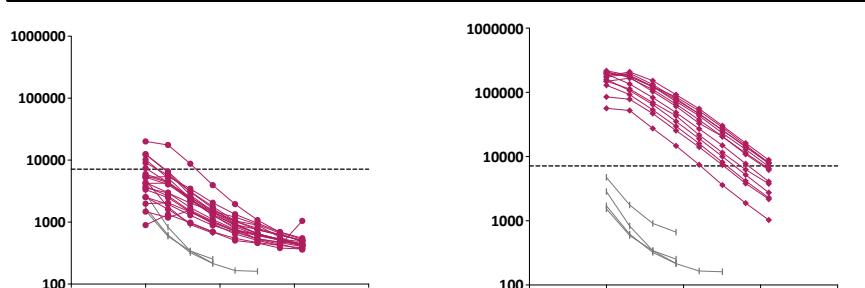
RBD - convalescent



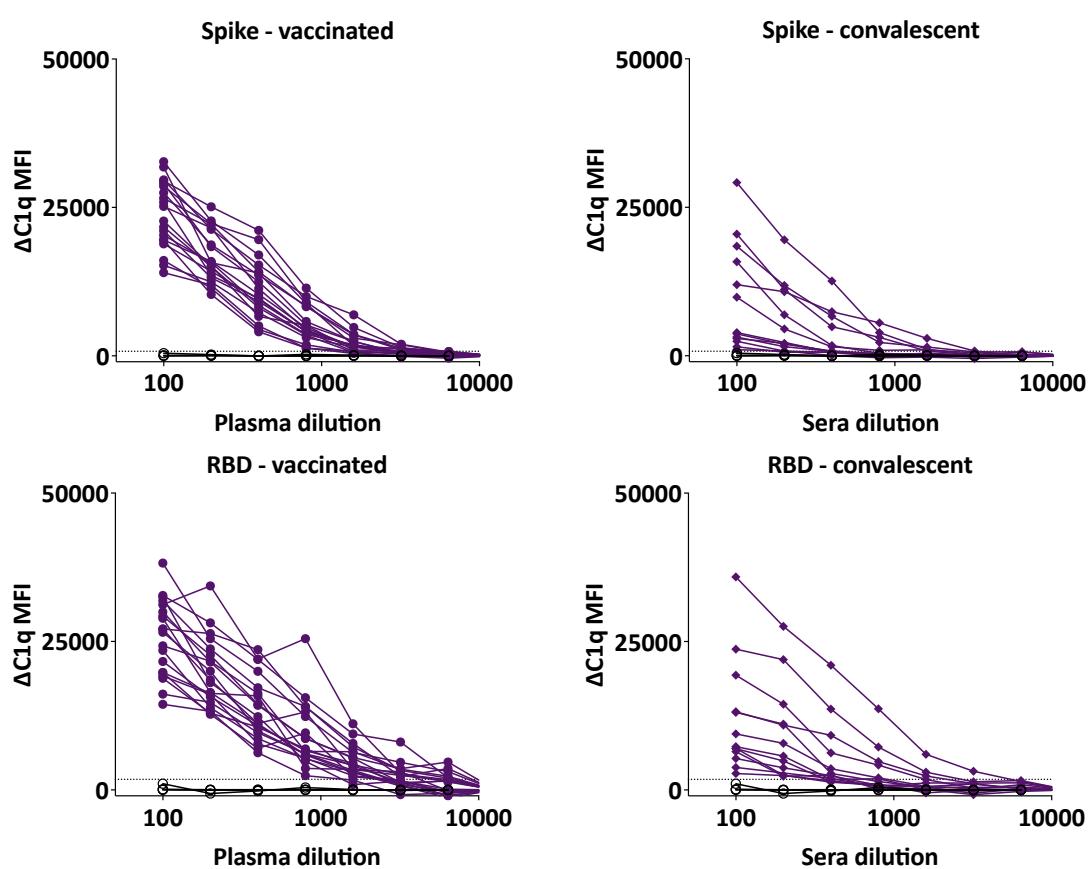
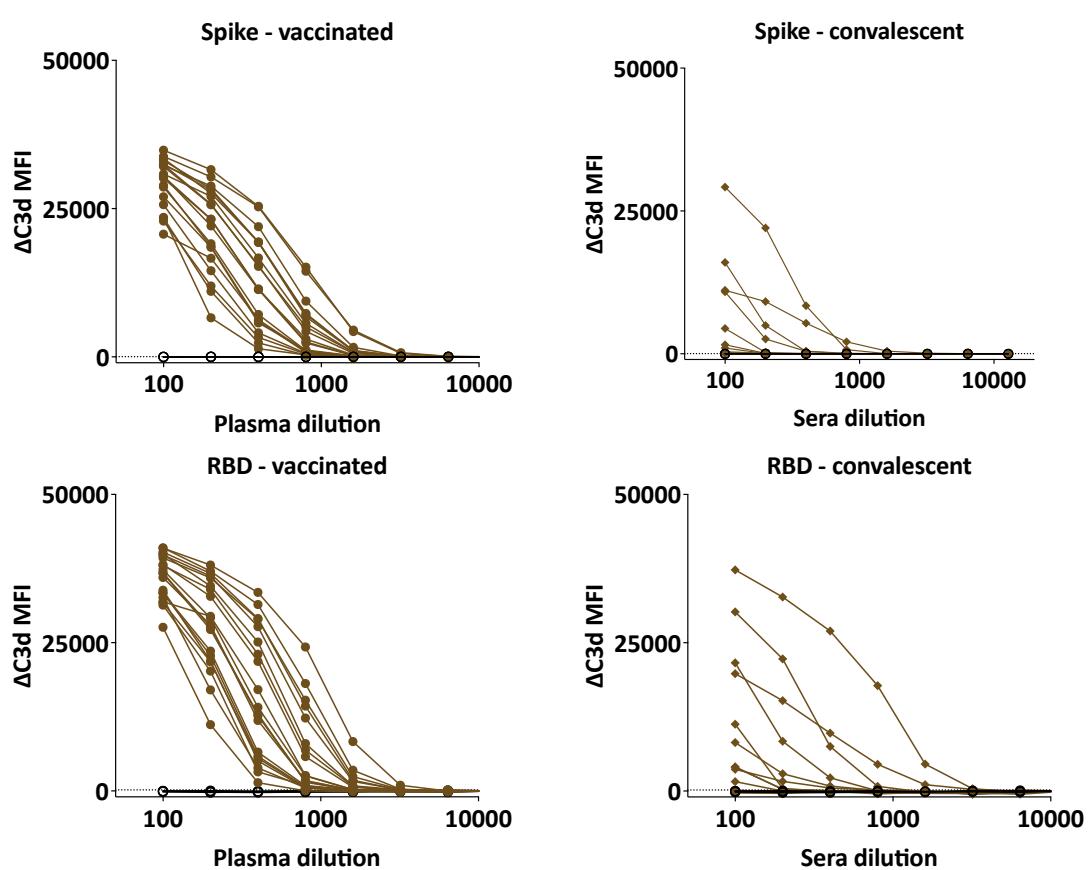
COVID-19-negative subjects

— Cutoff

**Supplemental Figure 4.** (A-B) C1q or C3d binding to RBD-specific Abs in plasma specimens from seven vaccinated individuals (left) and seven convalescent COVID-19 patients (right) and four COVID-19-negative controls. Specimens were diluted at 2-fold dilutions from 1:100 to 1:6,400 or 12,800. The dotted line represents the 100x dilution cut-off calculated as mean of the four control specimens + 3SD.  $\Delta$ C1q (A) and  $\Delta$ C3d (B) MFI values were calculated by subtracting background MFI from each assay.

**Vaccinated subjects****Convalescent patients****Spike****RBD****S1****S2****Nucleoprotein****Sera dilution****Plasma dilution**

**Supplemental Figure 5.** Titration curves are shown for total Ig against spike, RBD, S1, S2 and nucleoprotein in sera and plasma specimens from 20 vaccinated subjects (left panels), 13 convalescent COVID-19 patients (right panels) and four COVID-19-negative subjects (gray). Specimens were diluted at 4-fold dilutions from 1:100 to 1:12,800. The dotted lines indicated the cut-off values calculated as mean + 3SD of 1:100 diluted plasma of the four COVID-19-negative specimens. Data were generated using the multiplex bead antibody binding assay and mean fluorescent intensity (MFI) values were plotted.

**(A)****(B)**

○ COVID-19-negative subjects

— — Cutoff

**Supplemental Figure 6.** (A-B) C1q or C3d binding to spike- or RBD-specific Abs in plasma specimens from 20 vaccinated individuals (left) and 13 convalescent COVID-19 patients (right) and four COVID-19-negative controls. Specimens were diluted at 2-fold dilutions from 1:100 to 1:6,400 or 12,800. The dotted line represents the 100x dilution cut-off calculated as mean of the four control specimens + 3SD.  $\Delta$ C1q (A) and  $\Delta$ C3d (B) MFI values were calculated by subtracting background MFI from each assay.